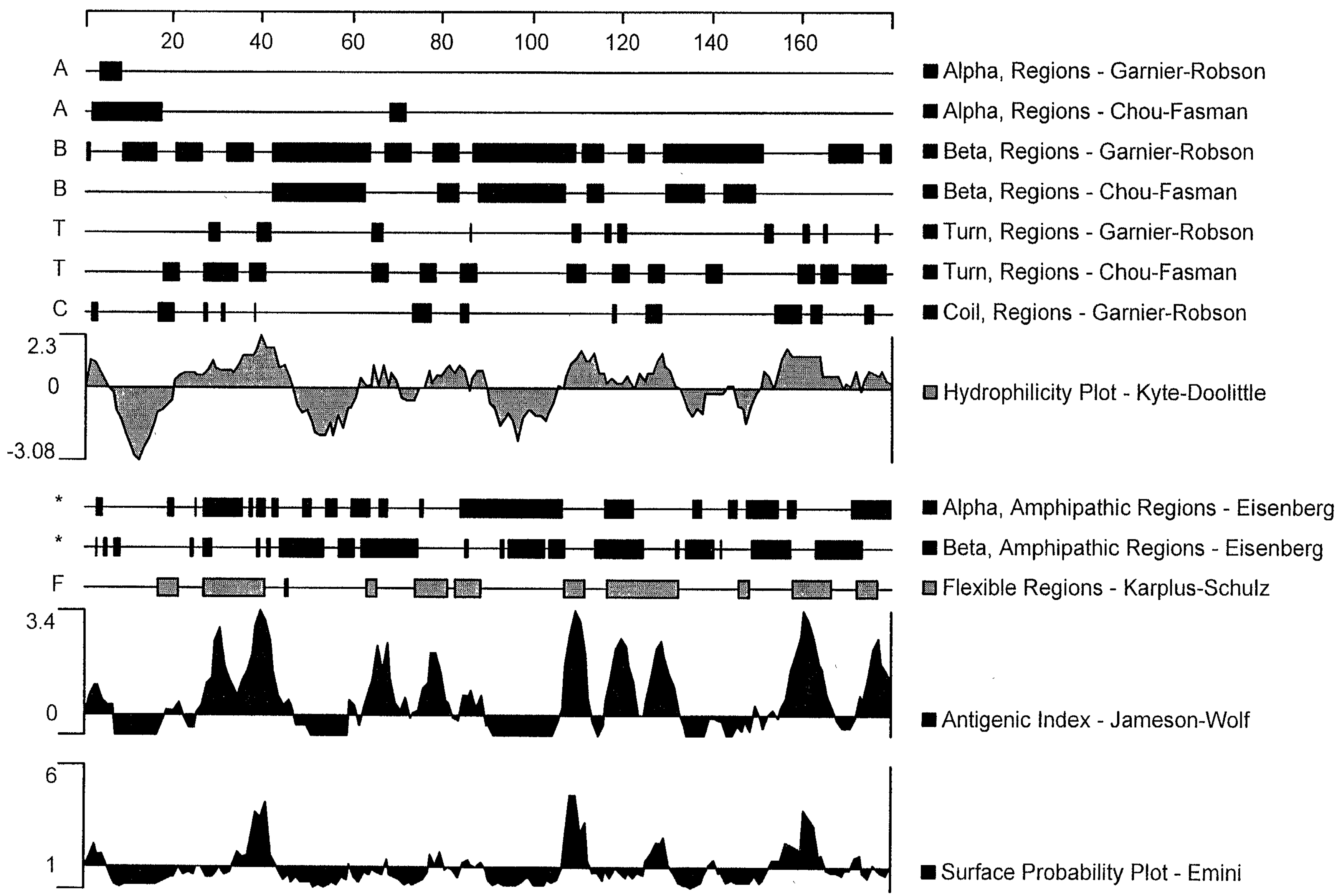
Figure 1
PSSP

```
                .         .         .         .         .         .
  1 GGCACGAGCCAGCTCCTTCCTGTTCCCCTGGCGGCCCCTCGCTTCTTCCTTCTGGATGGG   60

                .         .         .         .         .         .
 61 GGCCCAGGGGGCCCAGGAGAGTATAAAGGCGATGTGGAGGGTGCCCGGCACAACCAGACG  120

                .         .         .         .         .         .
121 CCCAGTCACAGGCGAGAGCCCTGGGATGCACCGGCCAGAGGCCATGCTGCTGCTGCTCAC  180
  1                           M  H  R  P  E  A  M  L  L  L  L  T   12

                .         .         .         .         .         .
181 GCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTATGGCCCTGGAGGAGGCAA  240
 13  L  A  L  L  G  G  P  T  W  A  G  K  M  Y  G  P  G  G  G  K   32

                .         .         .         .         .         .
241 GTATTTCAGCACCACTGAAGACTACGACCATGAAATCACAGGGCTGCGGGTGTCTGTAGG  300
 33  Y  F  S  T  T  E  D  Y  D  H  E  I  T  G  L  R  V  S  V  G   52

                .         .         .         .         .         .
301 TCTTCTGCTGGTGAAAAGTGTCCAGGTGAAACTTGGAGACTCCTGGGACGTGAAACTGGG  360
 53  L  L  L  V  K  S  V  Q  V  K  L  G  D  S  W  D  V  K  L  G   72

                .         .         .         .         .         .
361 AGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATACATCACAAAAGT  420
 73  A  L  G  G  N  T  Q  E  V  T  L  Q  P  G  E  Y  I  T  K  V   92

                .         .         .         .         .         .
421 CTTTGTCGCCTTCCAAGCTTTCCTCCGGGGTGTGGTCATGTACACCAGCAAGGACCGCTA  480
 93  F  V  A  F  Q  A  F  L  R  G  V  V  M  Y  T  S  K  D  R  Y  112

                .         .         .         .         .         .
481 TTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCCAGCCAAGAGGGGCA  540
113  F  Y  F  G  K  L  D  G  Q  I  S  S  A  Y  P  S  Q  E  G  Q  132

                .         .         .         .         .         .
541 GGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGCTTTGA  600
133  V  L  V  G  I  Y  G  Q  Y  Q  L  L  G  I  K  S  I  G  F  E  152

                .         .         .         .         .         .
601 ATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTCAGC  660
153  W  N  Y  P  L  E  E  P  T  T  E  P  P  V  N  L  T  Y  S  A  172

                .         .         .         .         .         .
661 AAACTCACCCGTGGGTCGCTAGGGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGGG  720
173  N  S  P  V  G  R  *                                         179

                .         .         .         .         .         .
721 TGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAAT  780

                .         .         .         .
781 AAATAAAGCTTCTGCAGAAAAAAAAAAAAAAAAAAAAAAAAAA                   825
```

Figure 2

```
                               10                  20                  30                  40
  1  M H R P E A M L L L L T L A L L G G P T - W A G K M Y - G P G G G K Y F S T T E  PSSP.AA
  1  M - - - - - - L P L L I L A F L G T P A V L T Q S R Y H G S E T G K H F C I V A  U00964.aa

                               50                  60                  70                  80
 39  D Y D H E I T G I R V S V G L L L V K S V Q V K L G D S W D V K L G A L G G N T  PSSP.AA
 35  P E G E P V T G I W A S I K N N I L S S I R L K F G N N W S Q E Y G S S G R A E  U00964.aa

                               90                 100                 110                 120
 79  Q E V T L Q P G E Y I T K V F V A F Q A F L R G V V M Y T S K D R Y F Y F G K L  PSSP.AA
 75  I E V K L N P D E T V L G F S G S F Y I F M H Q I I I T T S Q P R E L I I G P L  U00964.aa

                              130                 140                 150                 160
119  D G Q - I S S A Y P S Q E G Q V L V G I Y G Q Y Q L L G I K S I G F E W N Y P L  PSSP.AA
115  T G R Y V Y T S Y P E N P N H V F R G I C G Y Y V T G G L K G M R Y L W G - - -  U00964.aa

                              170                 180
158  E E P T T E P P V N L T Y S A N S P V G R .                                      PSSP.AA
152  - - - - - - - - N V N G T C T - - - - - - - - E                                  U00964.aa
```

Figure 3


20
40
60
80
100
120
140
160
A
A
B
B
T
T
C
2.3
0
-3.08
*
*
F
3.4
0
6
1
Alpha, Regions - Garnier-Robson
Alpha, Regions - Chou-Fasman
Beta, Regions - Garnier-Robson
Beta, Regions - Chou-Fasman
Turn, Regions - Garnier-Robson
Turn, Regions - Chou-Fasman
Coil, Regions - Garnier-Robson
Hydrophilicity Plot - Kyte-Doolittle
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
Flexible Regions - Karplus-Schulz
Antigenic Index - Jameson-Wolf
Surface Probability Plot - Emini